

SEQUENCE LISTING

<110> Ledbetter, Jeffrey

Hayden-Ledbetter, Martha

<120> Binding Domain-Immunoglobulin Fusion Proteins

<130> 390069.401

<140> US

<141> 2002-01-17

<150> US 09/765,208

<151> 2001-01-17

<160> 38

<170> PatentIn version 3.0

<210> 1

<211> 812

<212> DNA

<213> Artificial Sequence

<220>

<223> SYNTHETIC MOUSE SCFV FUSION GENE

<220>

<221> sig_peptide

<222> (13)..(78)

<220>
 <221> V_region
 <222> (79)..(396)
 <223> light chain variable region for anti-CD20 scFv

<220>
 <221> misc_feature
 <222> (397)..(444)
 <223> asp-gly3ser(gly4ser)2-ser peptide linker

<220>
 <221> V_region
 <222> (445)..(808)
 <223> heavy chain variable region for anti-CD20 scFv

<400> 1		
aagcttgcgg ccatggattt tcaagtgcag attttcagct tcctgctaatt cagtgcttca	60	
gtcataattt ccagaggaca aatttgttctc tcccagtcctc cagcaatccct gtctgcattct	120	
ccaggggaga aggtcacaat gacttgcagg gccagctcaa gtgttaatgttta catgcactgg	180	
taccacgaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctggct	240	
tctggagtcc ctgctcgctt cagttggcagt gggctggga cctcttactc tctcacaatc	300	
agcagagtggtt aggctgaaga tgctgccact tattactgcc agcagtggtt tttaaccca	360	
cccacgttcg gtgctgggac caagctggag ctgaaagggtg gcgggtggctc gggcggtgg	420	
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggt	480	
aggcctgggg cctcagtgaa gatgtcctgc aaggcttctg gctacacatt taccagttac	540	
aatatgcact gggtaaagca gacacctaga cagggctgg aatggattgg agctatttat	600	
ccagggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgtt	660	
gacaaatcct ccagcacagc ctacatgcag ctcagcagcc tgacatctga agactctgcg	720	
gtctatttctt gtgcaagagt ggtgtactat agtaactctt actggacttt cgatgtctgg	780	

ggcacagggca ccacggtcac cgtctctgat ca	812
<210> 2	
<211> 1518	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> SYNTHETIC MOUSE HUMAN CHIMERIC FUSION GENE	
<220>	
<221> misc_feature	
<222> (13)..(807)	
<223> MURINE ANTI-HUMAN CD20 scFv	
<220>	
<221> C_region	
<222> (808)..(1513)	
<223> HUMAN IgG1 Fc TAIL, WILD TYPE HINGE, CH2 AND CH3	
<400> 2	
aagcttgccg ccatggattt tcaagtgcag attttcagct tcctgctaatt cagtgcttca	60
gtcataatttgc ccagaggaca aatttgttctc tcccagtctc cagcaatcct gtctgcatttct	120
ccaggggaga aggtcacaat gacttgcagg gccagctcaa gtgttaatttta catgcactgg	180
taccaggcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctggct	240
tctggagtcc ctgtcgctt cagttggcagt gggcttggga ccttttactc ttcacaatc	300
agcagagtgg aggctgaaga tgctgccact tattactgcc agcagtggag tttaaccca	360
cccaacgttcg gtgtgggac caagctggag ctgaaagatg gcgggtggctc gggcggtgg	420
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctggtg	480
aggcctgggg cctcagtgaa gatgtcctgc aaggcttctg gctacacatt taccagttac	540
aatatgcact ggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat	600

ccagggaaatg	gtgatacttc	ctacaatcg	aagttcaagg	gcaaggccac	actgactgta	660
gacaaatcct	ccagcacagc	ctacatgcag	ctcagcagcc	tgacatctga	agactctgcg	720
gtctatttct	gtgcaagagt	ggtgtactat	agtaactctt	actggactt	cgttgtctgg	780
ggcacaggga	ccacggtcac	cgtctctgat	caggagccca	aatcttgtga	caaaaactcac	840
acatgcccac	cgtgcccagc	acctgaactc	ctggggggac	cgtcagtctt	cctttcccc	900
ccaaaaccca	aggacaccct	catgatctcc	cggaccctg	aggtcacatg	cgtggtggtg	960
gacgtgagcc	acgaagaccc	tgaggtcaag	ttcaactggt	acgtggacgg	cgtggaggtg	1020
cataatgcca	agacaaagcc	gcgggaggag	cagtacaaca	gcacgtaccg	tgtggtcagc	1080
gtcctcaccg	tcctgcacca	ggactggctg	aatggcaagg	agtacaagtg	caaggtctcc	1140
aacaaagccc	tcccagcccc	catcgagaaa	acaatctcca	aagccaaagg	gcagccccga	1200
gaaccacagg	tgtacaccct	gccccatcc	cgggatgagc	tgaccaagaa	ccaggtcagc	1260
ctgacctgcc	tggtcaaagg	cttctatccc	agcgacatcg	ccgtggagtg	ggagagcaat	1320
gggcagccgg	agaacaacta	caagaccacg	cctccgtgc	tggactccga	cggctcccttc	1380
ttcctctaca	gcaagctcac	cgtggacaag	agcaggtggc	agcagggaa	cgtttctca	1440
tgctccgtga	tgcatgaggc	tctgcacaac	cactacacgc	agaagagcct	ctccctgtct	1500
ccgggtaaat	gatctaga					1518

<210> 3

<211> 1518

<212> DNA

<213> Artificial Sequence

<220>

<223> SYNTHETIC MOUSE-HUMAN CHIMERIC FUSION GENE

<220>

<221> misc_feature

<222> (13)..(807)<223> MOUSE ANTI-HUMAN CD20 SCFV

<220>

<221> C_region

<222> (808)..(1513)

<223> HINGE CYSTEINES (826-829; 844-847; 853-856) MUTATED TO SERINES
 PROLINE TO SERINE MUTATION (880-883) IN CH2 DISRUPTS EFFECTOR FUNCTION

<400> 3	
aagcttgcgg ccatggattt tcaagtgcag attttcagct tcctgcta at cagtgc ttca	60
gtcataattt ccagaggaca aatttgttctc tcccagtctc cagaatcct gtctgc atct	120
ccagggaga aggtcacaat gacttgcagg gccagctcaa gtgtta aggtt catgcactgg	180
taccaggcaga agccaggatc ctccccaaa ccctggattt atgccccatc caacctggct	240
tctggagtcc ctgctcgctt cagttggcagt gggcttgga cctcttactc tctcacaatc	300
agcagagtgg aggctgaaga tgctgccact tattactgcc agcagtggag ttttaaccca	360
cccacgttcg gtgctggac caagctggag ctgaaagatg gcggtggctc gggcggtgg	420
ggatctggag gaggtggag ctctcaggct tatctacagc agtctgggc tgagctgg	480
aggcctgggg cctcagtgaa gatgtcctgc aaggcttctg gctacacatt taccagttac	540
aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat	600
ccagggaaatg gtgataacttc ctacaatcag aagttcaagg gcaaggccac actgactgta	660
gacaaatcct ccagcacagc ctacatgcag ctcagcagcc tgacatctga agactctgcg	720
gtcttatttct gtgcaagagt ggtgtactat agtaactctt actggtaactt cgatgtctgg	780
ggcacaggga ccacggtcac cgtctctgat caggagccca aatcttctga caaaactcac	840
acatccccac cgtccccac acctgaactc ctggggggat cgtcagtctt cctttcccc	900
ccaaaaccca aggacacct catgatctcc cggacccctg aggtcacatg cgtggtggtg	960
gacgtgagcc acgaagaccc tgaggtcaag ttcaactgg acgtggacgg cgtggaggtg	1020
cataatgccca agacaaagcc gcgggaggag cagtaacaaca gcacgtaccg tgtggtaagc	1080
gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc	1140
aacaaagccc tcccagcccc catcgagaaa acaatctcca aagccaaagg gcagccccga	1200
gaaccacagg tgtacaccct gccccatcc cgggatgagc tgaccaagaa ccaggtcagc	1260
ctgacccctgcc tggtaaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat	1320
gggcagccgg agaacaacta caagaccacg cctccctgc tggactccga cggctcccttc	1380

ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcagggaa cgtttctca	1440
tgctccgtga tgcataggc tctgcacaac cactacacgc agaagagcct ctccctgtct	1500
ccgggtaaat gatctaga	1518

<210> 4

<211> 1518

<212> DNA

<213> Artificial Sequence

<220>

<223> SYNTHETIC MOUSE-HUMAN CHIMERIC FUSION GENE

<220>

<221> misc_feature

<222> (13)..(807)

<223> MOUSE ANTI-HUMAN CD20 SCFV

<220>

<221> C_region

<222> (808)..(1513)

<223> HINGE CYSTEINES MUTATED TO SERINES (826-829; 844-847; 853-856)
WILD TYPE CH2 AND CH3 DOMAINS MEDIATE EFFECTOR FUNCTIONS

<400> 4

aagcttgcgg ccatggattt tcaagtgcag attttcagct tcctgctaatt cagtgcttca	60
--	----

gtcataattt ccagaggaca aattgttctc tcccagtctc cagcaatcct gtctgcattt	120
---	-----

ccagggaga aggtcacaat gacttgcagg gccagctcaa gtgttaatcatgcactgg	180
---	-----

taccaggcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctggct	240
--	-----

tctggagtcc ctgctcgctt cagttggcagt gggcttggga cctttactc tctcacaatc	300
---	-----

agcagagtgg aggctgaaga tgctgccact tattactgcc agcagtggag ttttaaccca	360
---	-----

cccacgttcg gtgttggac caagctggag ctgaaagatg gcgggtggctc gggcggtgg	420
--	-----

ggatctggag gaggtggag ctctcaggct tatctacagc agtctgggc tgagctggg 480
 aggctgggg cctcagtcaa gatgtcctgc aaggcttctg gctacacatt taccagttac 540
 aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600
 ccagggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660
 gacaaatcct ccagcacagc ctacatgcag ctcagcagcc tgacatctga agactctgcg 720
 gtcttatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780
 ggcacaggga ccacggtcac cgtctctgat caggagccca aatcttctga caaaaactcac 840
 acatccccac cgtccccagc acctgaactc ctggggggac cgtcagtctt cctttcccc 900
 ccaaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg 960
 gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 1020
 cataatgccca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 1080
 gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 1140
 aacaaagccc tcccagccccc catcgagaaa acaatctcca aagccaaagg gcagcccccga 1200
 gaaccacagg tgtacaccct gccccatcc cgggatgagc tgaccaagaa ccaggtcagc 1260
 ctgacctgcc tggtaaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 1320
 gggcagccgg agaacaacta caagaccacg cctccctgc tggactccga cggctccctc 1380
 ttccctctaca gcaagctcac cgtggacaag agcaggtggc agcagggaa cgtttctca 1440
 tgctccgtga tgcataggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1500
 ccgggtaaat gatctaga 1518

<210> 5

<211> 1524

<212> DNA

<213> Artificial Sequence

<220>

<223> SYNTHETIC MOUSE HUMAN CHIMERIC FUSION GENE

<220>

<221> misc_feature
<222> (1)..(796)
<223> MOUSE ANTI HUMAN CD20 SCFV

<220>
<221> N_region
<222> (797)..(864)
<223> HUMAN IGA HINGE REGION

<220>
<221> C_region
<222> (865)..(1518)
<223> HUMAN IGG1 CH2 AND CH3 WILD TYPE FC DOMAIN

<400>	5	
atggattttc aagtgcagat tttcagcttc ctgctaata	gtgcttcagt cataattgcc	60
agaggacaaa ttgttctctc ccagtctcca gcaatcctgt	ctgcatactcc aggggagaag	120
gtcacaatga cttgcagggc cagctcaagt gtaagttaca	tgcactggta ccagcagaag	180
ccagggatcct cccccaaacc ctggatttat gccccatcca	acctggcttc tggagtccct	240
gctcgcttca gtggcagtgg gtctgggacc tcctactctc	tcacaatcag cagagtggag	300
gctgaagatg ctgccactta ttactgccag cagtggagtt	ttaaccacc cacgttcggt	360
gctgggacca agctggagct gaaagatggc ggtggctcg	gcgggtggat atctggagga	420
ggtgtggagct ctcaggctta tctacagcag tctggggctg	agctggtgag gcctggggcc	480
tcaagtgaaga tgtcctgcaa ggcttctggc tacacattt	ccagttacaa tatgcactgg	540
gtaaaggcaga cacctagaca gggcctggaa tggattggag	ctattttatcc aggaaatggt	600
gatacttcct acaatcagaa gttcaagggc aaggccacac	tgactgtaga caaatcctcc	660
agcacacgcct acatgcagct cagcagcctg acatctgaag	actctgcggc ctatttctgt	720
gcaagagttgg tgtactatacg taactcttac tggtaacttcg	atgtctgggg cacaggacc	780
acggtcaccg tctctgatca gccagttccc tcaactccac	ctaccccatc tccctcaact	840
ccacctaccc catctccctc atgcgcaccc	gaactcctgg ggggaccgac	900

ttcccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 960
 gtggtggacg tgagccacga agacccttagt gtcagaattca actggtagt ggacggcgtg 1020
 gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg 1080
 gtcagcgtcc tcaccgtct gcaccaggac tggctgaatg gcaaggagta caagtgc当地 1140
 gtctccaaca aagccctccc agccccatc gagaaaaacaa tctccaaagc caaagggc当地 1200
 ccccgagaac cacaggtgta caccctgecc ccatccccgg atgagctgac caagaaccag 1260
 gtcagcctga cctgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtggag 1320
 agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1380
 tccttcttcc tctacagcaa gtcaccgtg gacaagagca ggtggcagca gggaaacgtc 1440
 ttctcatgct cctgtatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc 1500
 ctgtctccgg gtaaatgatc taga 1524

<210> 6

<211> 711

<212> DNA

<213> Artificial Sequence

<220>

<223> SYNTHETIC HUMAN PARTIAL FUSION GENE

<220>

<221> misc_feature
<222> (1)..(705)

<223> HINGE CYSTEINES MUTATED TO SERINES (19-21; 37-39; 46-48)

<400> 6
 gatcaggagc ccaaattttc tgacaaaact cacacatccc caccgtcccc agcacctgaa 60
 ctcctggggg gaccgtcagt cttcctttc ccccaaaaac ccaaggacac cctcatgatc 120
 tcccgaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc 180
 aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcggag 240
 gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 300

ctgaatggca aggagtacaa gtgcaaggc tccaaacaag ccctcccagc ccccatcgag 360
 aaaacaatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 420
 tcccggtatg agctgaccaa gaaccaggc agcctgacct gcctggtaa aggcttctat 480
 cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cgagaacaa ctacaagacc 540
 acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac 600
 aagagcaggt ggcagcaggg gaacgttttc tcatgctccg tcatgcatga ggctctgcac 660
 aaccactaca cgcagaagag cctctccctg tctccggta aatgatctag a 711

<210> 7

<211> 729

<212> DNA

<213> Artificial Sequence

<220>

<223> SYNTHETIC HUMAN PARTIAL FUSION GENE

<220>

<221> N_region

<222> (1)..(69)

<223> HUMAN IGA HINGE

<220>

<221> C_region

<222> (70)..(723)

<223> HUMAN WILD TYPE IGG1 CH2 AND CH3, FC

<400> 7

gatcagccag ttccctcaac tccacaccttcc ccatctccct caactccacc tacccatct 60
 ccctcatgcg cacctgaact cctggggggga ccgtcagtct tcctttccc cccaaaaccc 120
 aaggacaccc tcatgatctc ccggacccct gaggtcacat gcgtggtggt ggacgtgagc 180
 cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc 240

aagacaaagc cgcgggagga gcagtacaac agcacgtacc gtgtggtcag cgtcctcacc	300
gtcctgcacc aggactggct gaatggcaag gagtacaagt gcaaggcttc caacaaagcc	360
ctcccagccc ccatcgagaa aacaatctcc aaagccaaag ggcagccccg agaaccacag	420
gtgtacaccc tgccccatc ccgggatgag ctgaccaaga accaggtcag cctgacctgc	480
ctggtcaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa tggcagccg	540
gagaacaact acaagaccac gcctccgtg ctggactccg acggctcctt cttcctctac	600
agcaagctca ccgtggacaa gagcaggtgg cagcagggga acgtttctc atgctccgtg	660
atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tccggtaaa	720
tgatctaga	729

<210> 8
<211> 825
<212> DNA
<213> Artificial Sequence

<220>
<223> SYNTHETIC MOUSE SCFV FUSION GENE
<220>
<221> misc_feature
<222> (13)..(72)
<223> LIGHT CHAIN LEADER PEPTIDE

<220>
<221> V_region
<222> (73)..(405)
<223> LIGHT CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD19: HD37

<220>
<221> misc_feature

<222> (406)..(450)

<223> SYNTHETIC (GLY4SER)3 LINKER PEPTIDE

<220>

<221> V_region

<222> (454)..(825)

<223> HEAVY CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD19: HD37

<400> 8		
aagcttgcgg ccatggagac agacacactc ctgctatggg tgctgctgct ctgggttcca	60	
ggctccactg gtgacattgt gctgacccaa tctccagctt ctttgctgt gtctcttaggg	120	
cagagggcca ccatctcctg caaggccagc caaagtgtt attatgatgg tgatagttat	180	
ttgaactggt accaacagat tccaggacag ccacccaaac tcctcatcta tgatgcatcc	240	
aatctagttt ctgggatccc acccaggttt agtggcagtg ggtctggac agacttcacc	300	
ctcaacatcc atcctgtgga gaaggtggat gctgcaacct atcactgtca gcaaagtact	360	
gaggatccgt ggacgttcgg tggaggcacc aagctggaaa tcaaaggtgg cggtggctcg	420	
ggcggtgttg ggtcggttgg cggcggatcg tcacaggttc agctgcagca gtctgggct	480	
gagctggta ggcctgggtc ctcagtgaag atttcctgca aggcttctgg ctatgcattc	540	
agtagctact ggatqaactg ggtgaagcag aggcctggac agggtcttga gtggattgga	600	
cagatttggc ctggagatgg tgatactaac tacaatggaa agttcaaggg taaagccact	660	
ctgactgcag acgaatccctc cagcacagcc tacatgcaac tcagcagcct agcatctgag	720	
gactctgcgg tctatttctg tgcaagacgg gagactacga cggtaggccg ttattactat	780	
gctatggact actggggtca aggaacctca gtcaccgtct cctca	825	

<210> 9

<211> 795

<212> DNA

<213> Artificial Sequence

<220>

<223> SYNTHETIC MOUSE SCFV FUSION GENE

<220>

<221> misc_feature

<222> (13)..(72)

<223> LIGHT CHAIN LEADER PEPTIDE SEQUENCE

<220>

<221> V_region

<222> (73)..(393)

<223> LIGHT CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD37: G28-1

<220>

<221> misc_feature

<222> (394)..(441)

<223> SYNTHETIC LINKER PEPTIDE ENCODED (GLY4SER)3

<220>

<221> V_region

<222> (442)..(795)

<223> HEAVY CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD37: G28-1

<400> 9

aagcttgcgc ccatggtatac cacagctcag ttccttggt tgctgctgct gtggcttaca 60

ggtgtggcagat gtgacatcca gatgactcag tctccagcct ccctatctgc atctgtggga 120

gagactgtca ccatcacatg tcgaacaagt gaaaatgttt acagttattt ggcttggtat 180

cagcagaaac agggaaaatc tcctcagctc ctgggtcttt ttgcaaaaac cttagcagaa 240

ggtgtgtccat caagggttcag tggcagtggta tcaggcacac agttttctct gaagatcagc 300

agcctgcagc ctgaagattc tggaagttat ttctgtcaac atcattccga taatccgtgg 360

acgttcggtg gaggcaccga actggagatc aaaggtggcg gtggctcgaa cggtgggtgg 420

tcgggtggcg gcggatcgta agcggccag ctgcagcagt ctggacactga gctggaaaag 480

cctggcgctt cagtgaagat ttcctgcaag gcttctggtt actcattcac tggctacaat 540
atgaactggg tgaaggcagaa taatggaaag agccttgagt ggattggaaa tattgatcct 600
tattatggtg gtactaccta caaccggaag ttcaagggca aggccacatt gactgttagac 660
aaatcctcca gcacagccta catgcagctc aagagtctga catctgagga ctctgcagtc 720
tattactgtg caagatcggt cggccctatg gactactggg gtcaaggaac ctcagtcacc 780
gtctcttctg atcag 795

<210> 10

<211> 824

<212> DNA

<213> Artificial Sequence

<220>

<223> SYNTHETIC MOUSE FUSION GENE

<220>

<221> sig_peptide

<222> (1)..(61)

<223> native light chain leader peptide

<220>

<221> V_region

<222> (62)..(397)

<223> LIGHT CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD22: G28-7

<220>

<221> misc_feature

<222> (398)..(445)

<223> (gly4ser)3 linker peptide

<220>

<221> V_region
<222> (445)..(818)

<223> HEAVY CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD22: G28-7

<220>

<221> misc_feature
<222> (819)..(824)

<223> BclI restriction site

<400> 10		
atggagtcac attcccagg tttctctcc ctgctgtct ggttatctgg tacctgtggg	60	
aacattatga tgacacagtc gccatcatct ctggctgtgt cagcaggaga aaaggtca	120	
atgaactgta agtccagtca aagtgtttt tacagttcaa atcagaggaa ttatggcc	180	
tggtatcagc agaaaccagg gcagtctccc aaattgctga tctactgggc atctactagg	240	
gaatctggtg tccctgatcg cttcacaggc agtggatccg ggacagactt tactcttacc	300	
atcagcagt tacatactga agacctggca gtttattact gtcatcaatt cctctttcg	360	
tggacgttcg gtggaggcac caagctggaa atcaaaggcg gtgggttgc gggtggttgt	420	
ggttcgggtg cggcggtac ttctcaggc caactgcagc agcctgggc tgaactggtg	480	
aagcctggga cttagtcaa gctgtcctgc aaggcctctg gctacacctt caccaactac	540	
tggatggtct gggtaagca gacgcctgga gaaggccttg agtggattgg agaaattatt	600	
cctagcaacg gtcgtactaa atacaatgag aagttcaaga gcaaggccac actgactgca	660	
gacaaatcct cccgcacagc ctacatgcaa ctcagcagcc tggcatctga ggactctg	720	
gtctattatt gtgcaagaga gatgtccatt attactacgg tactgactcc cggttgctt	780	
actggggcca agggactctg gtcactgtct ctgcagcctg atca	824	

<210> 11

<211> 266

<212> PRT

<213> Mus musculus

<220>

<221> INIT_MET

<222> (1)..(1)

<220>

<221> SIGNAL

<222> (1)..(22)

<220>

<221> DOMAIN

<222> (23)..(128)

<223> LIGHT CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD20

<220>

<221> SITE

<222> (129)..(144)

<223> ASP-(GLY3SER)-(GLY4SER) 2-SER LINKER PEPTIDE

<220>

<221> DOMAIN

<222> (145)..(266)

<223> HEAVY CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD20

<400> 11

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15

Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20 25 30

Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45

Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser

50

55

60

Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95

Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110

Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125

Asp Gly Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser
 130 135 140

Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175

Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240

Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255

Gly Thr Gly Thr Thr Val Thr Val Ser Asp
 260 265

<210> 12

<211> 271

<212> PRT

<213> Mus musculus

<220>

<221> SITE

<222> (1)...(271)

<223> MOUSE ANTI-HUMAN CD19 SCFV

<400> 12

Met	Glu	Thr	Asp	Thr	Leu	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp	Val	Pro
1				5					10				15		
Gly	Ser	Thr	Gly	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ala
					20			25					30		
Val	Ser	Leu	Gly	Gln	Arg	Ala	Thr	Ile	Ser	Cys	Lys	Ala	Ser	Gln	Ser
					35			40			45				
Val	Asp	Tyr	Asp	Gly	Asp	Ser	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Ile	Pro
					50			55			60				
Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Asp	Ala	Ser	Asn	Leu	Val	Ser
					65			70			75			80	
Gly	Ile	Pro	Pro	Arg	Phe	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr		
					85			90			95				
Leu	Asn	Ile	His	Pro	Val	Glu	Lys	Val	Asp	Ala	Ala	Thr	Tyr	His	Cys
					100			105				110			
Gln	Gln	Ser	Thr	Glu	Asp	Pro	Trp	Thr	Phe	Gly	Gly	Thr	Lys	Leu	
					115			120			125				
Glu	Ile	Lys	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly		
					130			135			140				
Gly	Ser	Ser	Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg
					145			150			155			160	
Pro	Gly	Ser	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ala	Phe
					165			170				175			
Ser	Ser	Tyr	Trp	Met	Asn	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu
					180			185			190				
Glu	Trp	Ile	Gly	Gln	Ile	Trp	Pro	Gly	Asp	Gly	Asp	Thr	Asn	Tyr	Asn
					195			200			205				
Gly	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Glu	Ser	Ser	Ser
					210			215			220				
Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Ala	Ser	Glu	Asp	Ser	Ala	Val
					225			230			235			240	
Tyr	Phe	Cys	Ala	Arg	Arg	Glu	Thr	Thr	Val	Gly	Arg	Tyr	Tyr	Tyr	
					245			250			255				
Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	
					260			265			270				

<210> 13
<211> 259
<212> PRT
<213> Mus musculus

<220>

<221> SITE
<222> (1)..(259)
<223> MOUSE ANTI-HUMAN CD37 SCFV

<400> 13

Met	Val	Ser	Thr	Ala	Gln	Phe	Leu	Gly	Leu	Leu	Leu	Trp	Leu	Thr		
1				5				10				15				
Gly	Gly	Arg	Cys	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ser	
		20					25					30				
Ala	Ser	Val	Gly	Glu	Thr	Val	Thr	Ile	Thr	Cys	Arg	Thr	Ser	Glu	Asn	
	35					40				45						
Val	Tyr	Ser	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Gln	Gly	Lys	Ser	Pro	
	50				55				60							
Gln	Leu	Leu	Val	Ser	Phe	Ala	Lys	Thr	Leu	Ala	Glu	Gly	Val	Pro	Ser	
65				70				75			80					
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Gln	Phe	Ser	Leu	Lys	Ile	Ser	
	85					90				95						
Ser	Leu	Gln	Pro	Glu	Asp	Ser	Gly	Ser	Tyr	Phe	Cys	Gln	His	His	Ser	
	100				105						110					
Asp	Asn	Pro	Trp	Thr	Phe	Gly	Gly	Thr	Glu	Leu	Glu	Ile	Lys	Gly		
	115				120				125							
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser	Ala		
130				135				140								
Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Glu	Lys	Pro	Gly	Ala	Ser	
145				150				155			160					
Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ser	Phe	Thr	Gly	Tyr	Asn	
	165					170			175							
Met	Asn	Trp	Val	Lys	Gln	Asn	Asn	Gly	Lys	Ser	Leu	Glu	Trp	Ile	Gly	
	180					185			190							

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
 195 200 205

Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met
 210 215 220

Gln Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
 225 230 235 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
 245 250 255

Val Ser Ser

<210> 14

<211> 272

<212> PRT

<213> Mus musculus

<220>

<221> SITE

<222> (1)..(272)

<223> MOUSE ANTI-HUMAN CD22 SCFV

<400> 14

Met Glu Ser His Ser Gln Val Phe Leu Ser Leu Leu Leu Trp Val Ser
 1 5 10 15

Gly Thr Cys Gly Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala
 20 25 30

Val Ser Ala Gly Glu Lys Val Thr Met Asn Cys Lys Ser Ser Gln Ser
 35 40 45

Val Phe Tyr Ser Ser Asn Gln Arg Asn Tyr Leu Ala Trp Tyr Gln Gln
 50 55 60

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
 65 70 75 80

Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
 85 90 95

Phe Thr Leu Thr Ile Ser Ser Val His Thr Glu Asp Leu Ala Val Tyr
 100 105 110

Tyr Cys His Gln Phe Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys
 115 120 125

Leu Glu Ile Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
 130 135 140

Gly Gly Ser Ser Gln Val Gln Gln Pro Gly Ala Glu Leu Val
 145 150 155 160

Lys Pro Gly Thr Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr
 165 170 175

Phe Thr Asn Tyr Trp Met Val Trp Val Lys Gln Thr Pro Gly Glu Gly
 180 185 190

Leu Glu Trp Ile Gly Glu Ile Ile Pro Ser Asn Gly Arg Thr Lys Tyr
 195 200 205

Asn Glu Lys Phe Lys Ser Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser
 210 215 220

Arg Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala
 225 230 235 240

Val Tyr Tyr Cys Ala Arg Glu Met Ser Ile Ile Thr Thr Val Leu Thr
 245 250 255

Pro Gly Leu Leu Thr Gly Ala Lys Gly Leu Trp Ser Leu Ser Leu Gln
 260 265 270

<210> 15

<211> 499

<212> PRT

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>

<221> SITE

<222> (1)..(265)

<223> MOUSE ANTI-HUMAN CD20 SCFV: 2H7

<220>

<221> DOMAIN

<222> (266)..(499)
 <223> HUMAN IGG1 WILD TYPE HINGE, CH2, CH3 FC

<400> 15

Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser
1				5					10					15	
Val	Ile	Ile	Ala	Arg	Gly	Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ala	Ile
				20				25					30		
Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser
				35			40					45			
Ser	Ser	Val	Ser	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser
				50			55				60				
Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Pro	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro
	65				70				75					80	
Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile
				85				90					95		
Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp
				100				105					110		
Ser	Phe	Asn	Pro	Pro	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys
				115				120					125		
Asp	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Ser		
	130				135						140				
Gln	Ala	Tyr	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ala
	145				150				155				160		
Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr
				165				170					175		
Asn	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Arg	Gln	Gly	Leu	Glu	Trp	Ile
				180			185					190			
Gly	Ala	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Thr	Ser	Tyr	Asn	Gln	Lys	Phe
				195			200					205			
Lys	Gly	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr
				210			215					220			
Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys
	225				230				235					240	
Ala	Arg	Val	Val	Tyr	Tyr	Ser	Asn	Ser	Tyr	Trp	Tyr	Phe	Asp	Val	Trp
				245				250					255		
Gly	Thr	Gly	Thr	Thr	Val	Thr	Val	Ser	Asp	Gln	Glu	Pro	Lys	Ser	Cys

260

265

270

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 275 280 285

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 290 295 300

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 305 310 315 320

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 325 330 335

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 340 345 350

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 355 360 365

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 370 375 380

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 385 390 395 400

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 405 410 415

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 420 425 430

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 435 440 445

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 450 455 460

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 465 470 475 480

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 485 490 495

Pro Gly Lys

<210> 16

<211> 499

<212> PRT

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>

<221> SITE

<222> (1)..(265)

<223> 2H7 SCFV TARGETED TO HUMAN CD20

<220>

<221> DOMAIN

<222> (265)..(499)

<223> HINGE CYSTEINES MUTATED TO SERINES (AMINO ACIDS 272, 278, 281)
PROLINE IN CH2 MUTATED TO SERINE (AMINO ACID 290)

<400> 16

Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser
1				5					10					15	

Val	Ile	Ile	Ala	Arg	Gly	Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ala	Ile
				20				25					30		

Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser
				35			40					45			

Ser	Ser	Val	Ser	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser
				50			55				60				

Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Pro	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro
65				70					75				80		

Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile
				85				90				95			

Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp
				100				105				110			

Ser	Phe	Asn	Pro	Pro	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys
	115					120					125				

Asp	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser
130				135					140					

Gln	Ala	Tyr	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ala
145				150					155			160			

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser Ser
 260 265 270
 Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly
 275 280 285
 Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 290 295 300
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His
 305 310 315 320
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 325 330 335
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 340 345 350
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 355 360 365
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 370 375 380
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 385 390 395 400
 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 405 410 415
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 420 425 430
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 435 440 445
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 450 455 460

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 465 470 475 480

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 485 490 495

Pro Gly Lys

<210> 17

<211> 499

<212> PRT

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>

<221> SITE

<222> (1)..(265)

<223> MOUSE ANTI-HUMAN CD20 SCFV: 2H7

<220>

<221> DOMAIN

<222> (266)..(499)

<223> HINGE CYSTEINES MUTATED TO SERINES (AMINO ACIDS 272, 278, 281)
 CH2 AND CH3 DOMAINS ARE WILD TYPE IN SEQUENCE

<400> 17

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15

Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30

Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45

Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60

Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95

Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110

Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125

Asp Gly Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser
 130 135 140

Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175

Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240

Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255

Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser Ser
 260 265 270

Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly
 275 280 285

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 290 295 300

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 305 310 315 320

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 325 330 335

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 340 345 350

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 355 360 365

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 370 375 380

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 385 390 395 400

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 405 410 415

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 420 425 430

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 435 440 445

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 450 455 460

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 465 470 475 480

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 485 490 495

Pro Gly Lys

<210> 18

<211> 505

<212> PRT

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN FUSION PROTEIN

<220>

<221> SITE

<222> (1)..(265)

<223> MOUSE ANTI-HUMAN CD20 SCFV: 2H7

<220>

<221> DOMAIN

<222> (266)..(288)

<223> WILD TYPE IGA HINGE

<220>

<221> DOMAIN
 <222> (289)..(505)

<223> HUMAN IGG1 CH2 AND CH3 DOMAINS, WILD TYPE SEQUENCE

<400> 18

Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser
1				5					10					15	
Val	Ile	Ile	Ala	Arg	Gly	Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ala	Ile
				20				25					30		
Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser
					35		40					45			
Ser	Ser	Val	Ser	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser
					50		55				60				
Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Pro	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro
					65		70		75				80		
Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile
					85		90						95		
Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp
					100		105						110		
Ser	Phe	Asn	Pro	Pro	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys
					115		120						125		
Asp	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser	Ser	
					130		135						140		
Gln	Ala	Tyr	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ala
					145		150						160		
Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr
					165		170						175		
Asn	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Arg	Gln	Gly	Leu	Glu	Trp	Ile
					180		185						190		
Gly	Ala	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Thr	Ser	Tyr	Asn	Gln	Lys	Phe
					195		200						205		
Lys	Gly	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr
					210		215						220		
Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys

225	230	235	240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp			
245		250	255
Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Pro Val Pro Ser Thr			
260		265	270
Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys			
275		280	285
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys			
290		295	300
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val			
305		310	315
320			
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr			
325		330	335
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu			
340		345	350
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His			
355		360	365
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys			
370		375	380
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln			
385		390	395
400			
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu			
405		410	415
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro			
420		425	430
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn			
435		440	445
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu			
450		455	460
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val			
465		470	475
480			
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln			
485		490	495
Lys Ser Leu Ser Leu Ser Pro Gly Lys			
500		505	

<210> 19

<211> 234

<212> PRT

<213> Homo sapiens

<220>

<221> DOMAIN

<222> (1)..(234)

<223> MUTANT IGG1 HINGE (AMINO ACIDS 7, 13, 16)
WILD TYPE CH2 AND CH3 DOMAINS
ALTERNATIVE CARBOXY TERMINUS OF SCFVIG FUSION PROTEINS

<400> 19

Asp	Gln	Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser
1															
				5					10						15

Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro
				20				25							30

Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys
				35			40								45

Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp
			50			55						60			

Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu
	65			70			75						80		

Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu
				85				90					95		

His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn
			100			105						110			

Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly
	115					120						125			

Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu
	130					135						140			

Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr
	145				150			155					160		

Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn
		165				170						175			

Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe
		180			185							190			

Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn
		195			200							205			

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
210 215 220

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 20

<211> 240

<212> PRT

<213> Homo sapiens

<220>

<221> SITE
<222> (1)..(23)

<223> ALTERNATIVE CARBOXY TERMINUS OF SCFVIG FUSION PROTEINS

<220>

<221> DOMAIN
<222> (24)..(240)
<223> HUMAN IGG1 WILD TYPE CH2 AND CH3 FC

<400> 20

Asp Gln Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro
1 5 10 15

Pro Thr Pro Ser Pro Ser Cys Ala Pro Glu Leu Leu Gly Gly Pro Ser
20 25 30

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
35 40 45

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
50 55 60

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
65 70 75 80

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
85 90 95

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 100 105 110

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
 115 120 125

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 130 135 140

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
 145 150 155 160

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 165 170 175

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 180 185 190

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 195 200 205

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 210 215 220

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 225 230 235 240

<210> 21

<211> 1470

<212> DNA

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID

<220>

<221> misc_feature

<222> (1)..(808)

<223> MOUSE ANTI-HUMAN CD20 SCFV

<220>

<221> misc_feature

<222> (814)..(1455)

<223> HUMAN EXTRACELLULAR DOMAIN LONG FORM, CD154

© 2013 The Authors
Journal compilation
© 2013 British
Ecological Society,
Journal of Ecology,
101, 33–45

<400>	21					
aagcttgcgg	ccatggattt	tcaagtgcag	attttcagct	tcctgctaatt	cagtgcattca	60
gtcataattt	ccagaggaca	aatttgttctc	tcccagtctc	cagcaatcct	gtctgcattct	120
ccagggaga	aggtcacaat	gacttgcagg	gccagctcaa	gtgttaagtta	catgcactgg	180
taccagcaga	agccaggatc	ctcccccaaa	ccctggattt	atgccccatc	caacctggct	240
tctggagtcc	ctgctcgctt	cagtggcagt	gggtctggga	cctcttactc	tctcacaatc	300
agcagagtgg	aggctgaaga	tgctgccact	tattactgcc	agcagtggag	ttttaaccca	360
cccacgttcg	gtgctgggac	caagctggag	ctgaaaagatg	gcgggtggctc	gggcgggtgg	420
ggatctggag	gaggtgggag	ctctcaggct	tatctacagc	agtctggggc	tgagctggtg	480
aggcctgggg	cctcagtgaa	gatgtcctgc	aaggcttctg	gctacacatt	taccagttac	540
aatatgcact	gggttaaagca	gacacctaga	cagggcctgg	aatggattgg	agctatttat	600
ccagggaaatg	gtgataacttc	ctacaatcag	aagttcaagg	gcaaggccac	actgactgt	660
gacaaatcct	ccagcacagc	ctacatgcag	ctcagcagcc	tgacatctga	agactctgcg	720
gtcttatttct	gtgcaagagt	ggtgtactat	agtaactctt	actggtactt	cgatgtctgg	780
ggcacaggga	ccacggtcac	cgtctctgat	ccaagaaggt	tggacaagat	agaagatgaa	840
aggaatcttc	atgaagattt	tgtattcatg	aaaacgatac	agagatgcaa	cacaggagaa	900
agatccttat	ccttactgaa	ctgtgaggag	attaaaagcc	agtttgaagg	ctttgtgaag	960
gatataatgt	taaacaaaga	ggagacgaag	aaagaaaaca	gctttgaaat	gcaaaaaggt	1020
gatcagaatc	ctcaaattgc	ggcacatgtc	ataagtgagg	ccagcagtaa	aacaacatct	1080
gtgttacagt	gggctgaaaa	aggatactac	accatgagca	acaacttggt	aaccctggaa	1140
aatggaaac	agctgaccgt	taaaagacaa	ggactctatt	atatctatgc	ccaagtcacc	1200
ttctgttcca	atcgggaagc	ttcgagtcaa	gctccattta	tagccagcct	ctgcctaaag	1260
tcccccgta	gattcgagag	aatcttactc	agagctgcaa	atacccacag	ttccgccaaa	1320
ccttgcgggc	aacaatccat	tcacttggga	ggagtatttg	aattgcaacc	aggtgcttcg	1380
gtgtttgtca	atgtgactga	tccaagccaa	gtgagccatg	gcactggctt	cacgtccctt	1440
ggcttactca	aactcgagtg	ataatctaga				1470

<210> 22

<211> 1290
<212> DNA
<213> Artificial Sequence

<220>
<223> MOUSE-HUMAN HYBRID

<220>
<221> misc_feature
<222> (13)..(808)
<223> MOUSE ANTI-HUMAN CD20 SCFV

<220>
<221> misc_feature
<222> (814)..(1275)
<223> HUMAN EXTRACELLULAR DOMAIN, SHORT FORM, CD154

<400> 22		
aagcttgcgg ccatggattt tcaagtgcag attttcagct tcctgctaatt cagtgcttca	60	
gtcataattt ccagaggaca aatttgttctc tcccagtcctc cagcaatccgt gtctgcattt	120	
ccagggaga aggtcacaat gacttgcagg gccagctcaa gtgttaattt catgcactgg	180	
taccaggcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctggct	240	
tctggagtcc ctgctcgctt cagttggcagt gggctggga cctcttactc tctcacaatc	300	
agcagagtgg aggctgaaga tgctgccact tattactgcc agcagtggag tttaaccca	360	
cccacgttcg gtgctggac caagctggag ctgaaagatg gcggggctc gggcggtgg	420	
ggatctggag gaggtggag ctctcaggct tatctacagc agtctgggc tgagctgg	480	
aggcctgggg cctcagtgaa gatgtcctgc aaggcttctg gctacacatt taccagttac	540	
aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat	600	
ccagggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta	660	
gacaaaatcct ccagcacagc ctacatgcag ctcagcagcc tgacatctga agactctg	720	
gtcttatttct gtgcaagagt ggtgtactat agtaactctt actggactt cgatgtctgg	780	

Sequence Data from GenBank

ggcacaggga ccacggtcac cgtctctgat ccagaaaaca gcttgaaat gaaaaaggt 840
 gatcagaatc ctcaaattgc ggcacatgtc ataagtgagg ccagcagtaa aacaacatct 900
 gtgttacagt gggctgaaaa aggatactac accatgagca acaacttggt aaccctggaa 960
 aatggaaac agctgaccgt taaaagacaa ggactctatt atatctatgc ccaagtcacc 1020
 ttctgttcca atcgggaagc ttcgagtcaa gctccattta tagccagcct ctgcctaaag 1080
 tccccggta gattcgagag aatcttactc agagctgcaa atacccacag ttccgccaaa 1140
 ccttgcgggc aacaatccat tcacttggga ggagtattt aattgcaacc aggtgcttcg 1200
 gtgttgtca atgtgactga tccaagccaa gtgagccatg gcactggctt cacgtccctt 1260
 ggcttactca aactcgagtg ataatctaga 1290

<210> 23

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 23
 gtcaagcttg ccgccatgga ttttcaagtg cagattttc agc 43

<210> 24

<211> 74

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 24
 gtcgtcgagc tcccacctcc tccagatcca ccaccgcccc agccaccgccc acctttcagc 60

tccagcttgg tccc

74

<210> 25

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 25

gctgctgagc tctcaggctt atctacagca agtctgg

37

<210> 26

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 26

gttgtctgat cagagacggt gaccgtggtc cc

32

<210> 27

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 27

gttgtcggat ccagaaaaca gctttgaaat gcaa 34

<210> 28

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

gttgtttcta gattatcact cgagtttgag taagccaaag gacg 44

<400> 28

<210> 29

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

gttgtcggat ccaagaagg tggacaagat agaag 35

<400> 29

<210> 30

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 30

gtcttatataa gcagagctct ggc 23

<210> 31

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 31
cgaggctgat cagcgagotc tagca 25

<210> 32

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 32
ccgcaatttg aggattctga tcacc 25

<210> 33

<211> 482

<212> PRT

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>

<221> SITE
 <222> (1)..(266)
 <223> MOUSE ANTI-HUMAN CD20 SCFV

<220>

<221> DOMAIN
 <222> (268)..(481)
 <223> EXTRACELLULAR DOMAIN, LONG FORM, HUMAN CD154

<400> 33

Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser	
1															15	
Val	Ile	Ile	Ala	Arg	Gly	Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ala	Ile	
															30	
Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	
															45	
Ser	Ser	Val	Ser	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser	
															60	
Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Pro	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	
															80	
Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	
															95	
Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	
															110	
Ser	Phe	Asn	Pro	Pro	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys	
															125	
Asp	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser		
															140	
Gln	Ala	Tyr	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ala	
															160	
Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr	
															175	
Asn	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Arg	Gln	Gly	Leu	Glu	Trp	Ile	
															190	
Gly	Ala	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Thr	Ser	Tyr	Asn	Gln	Lys	Phe	

195

200

205

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240

Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255

Gly Thr Gly Thr Val Thr Val Ser Asp Pro Arg Arg Leu Asp Lys
 260 265 270

Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val Phe Met Lys Thr
 275 280 285

Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser Leu Leu Asn Cys
 290 295 300

Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys Asp Ile Met Leu
 305 310 315 320

Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu Met Gln Lys Gly
 325 330 335

Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser
 340 345 350

Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr Met
 355 360 365

Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys
 370 375 380

Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn
 385 390 395 400

Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys
 405 410 415

Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr His
 420 425 430

Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val
 435 440 445

Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro
 450 455 460

Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys
 465 470 475 480

Leu Glu

<210> 34
<211> 422
<212> PRT
<213> Artificial Sequence

<220>
<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>
<221> SITE
<222> (1)..(266)
<223> MOUSE ANTI-HUMAN SCFV

<220>
<221>
DOMAIN
<222> (268)..(421)
<223> EXTRACELLULAR DOMAIN, SHORT FORM, HUMAN CD154

<400> 34

Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser
1				5					10				15		

Val	Ile	Ile	Ala	Arg	Gly	Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ala	Ile
							20		25			30			

Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser
							35		40		45				

Ser	Ser	Val	Ser	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser
					50		55			60					

Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Pro	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro
65				70					75			80			

Ala	Arg	Phe	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile		
							85		90		95				

Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp
							100		105			110			

Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125

Asp Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser
 130 135 140

Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175

Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240

Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255

Gly Thr Gly Thr Thr Val Thr Val Ser Asp Pro Glu Asn Ser Phe Glu
 260 265 270

Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser
 275 280 285

Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly
 290 295 300

Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln
 305 310 315 320

Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr
 325 330 335

Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser
 340 345 350

Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala
 355 360 365

Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His
 370 375 380

Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn
 385 390 395 400

Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe
 405 410 415

Gly Leu Leu Lys Leu Glu
420

<210> 35

<211> 63

<212> DNA

<213> Homo sapiens

<220>

<221> N_region
<222> (1)..(63)

<223> PORTION OF HUMAN IGA HINGE DOMAIN CONTAINING ONLY 1 CYSTEINE

<400> 35

ccagttccct caactccacc taccccatct ccctcaactc cacctacccc atctccctca 60

tgc

63

<210> 36

<211> 21

<212> PRT

<213> Homo sapiens

<400> 36

Pro	Val	Pro	Ser	Thr	Pro	Pro	Thr	Pro	Ser	Pro	Ser	Thr	Pro	Pro	Thr
1				5				10				15			

Pro	Ser	Pro	Ser	Cys
			20	

<210> 37

<211> 763

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature
<222> (1)..(6)

<223> BCLI SITE FOR FUSION TO AMIN TERMINAL SCFVS

<220>

<221> N_region
<222> (8)..(752)<223> WILD TYPE IGA HINGE, CH2, CH3 DOMAINS
TRUNCATED TO REMOVE SECRETORY COMPONENT ATTACHMENT

<400> 37		
tgatcagcca gttccctcaa ctccacctac cccatctccc tcaactccac ctaccccatc	60	
tccctcatgc tgccacccccc gactgtcact gcaccgaccg gccctcgagg acctgcttt	120	
aggttcagaa gcgatcctca cgtgcacact gaccggcctg agagatgcct caggtgtcac	180	
cttcacctgg acgcccctcaa gtgggaagag cgctgttcaa ggaccacctg accgtgacct	240	
ctgtggctgc tacagcgtgt ccagtgtctt gccgggctgt gccgagccat ggaaccatgg	300	
gaagaccttc acttgcactg ctgcctaccc cgagtccaaag accccgctaa cccgcacccct	360	
ctcaaaatcc ggaaacacat tccggcccgaa ggtccacctg ctgccgccccgc cgtcggagga	420	
gctggccctg aacgagctgg tgacgctgac gtgcctggca cgtggcttca gccccaaagga	480	
tgtgctggtt cgctggctgc aggggtcaca ggagctgccc cgcgagaagt acctgacttg	540	
ggcatcccgga caggagccca gccagggcac caccacccctc gctgtgacca gcatactgcg	600	
cgtggcagcc gaggactgga agaagggggaa caccttctcc tgcattgggg gccacgaggc	660	
cctggccctg gcttcacac agaagaccat cgaccgcttgc gcggtaaac ccacccatgt	720	
caatgtgtct gttgtcatgg cgagggtggaa ctgataatct aga	763	

<210> 38

<211> 250

<212> PRT

<213> Homo sapiens

<220>

<221> DOMAIN

<222> (3)..(250)

<223> TRUNCATED FORM, REMOVAL OF LAST THREE AMINO ACIDS THAT MEDIATE ATTACHMENT TO SECRETORY COMPOUN

<400> 38

Asp	Gln	Pro	Val	Pro	Ser	Thr	Pro	Pro	Thr	Pro	Ser	Pro	Ser	Thr	Pro
1				5				10						15	
Pro	Thr	Pro	Ser	Pro	Ser	Cys	Cys	His	Pro	Arg	Leu	Ser	Leu	His	Arg
	20					25								30	
Pro	Ala	Leu	Glu	Asp	Leu	Leu	Leu	Gly	Ser	Glu	Ala	Ile	Leu	Thr	Cys
	35				40									45	
Thr	Leu	Thr	Gly	Leu	Arg	Asp	Ala	Ser	Gly	Val	Thr	Phe	Thr	Trp	Thr
	50				55						60				
Pro	Ser	Ser	Gly	Lys	Ser	Ala	Val	Gln	Gly	Pro	Pro	Asp	Arg	Asp	Leu
	65				70				75					80	
Cys	Gly	Cys	Tyr	Ser	Val	Ser	Ser	Val	Leu	Pro	Gly	Cys	Ala	Glu	Pro
		85				90								95	
Trp	Asn	His	Gly	Lys	Thr	Phe	Thr	Cys	Thr	Ala	Ala	Tyr	Pro	Glu	Ser
	100					105						110			
Lys	Thr	Pro	Leu	Thr	Ala	Thr	Leu	Ser	Lys	Ser	Gly	Asn	Thr	Phe	Arg
	115					120						125			
Pro	Glu	Val	His	Leu	Leu	Pro	Pro	Pro	Ser	Glu	Glu	Leu	Ala	Leu	Asn
	130				135					140					
Glu	Leu	Val	Thr	Leu	Thr	Cys	Leu	Ala	Arg	Gly	Phe	Ser	Pro	Lys	Asp
	145				150				155					160	
Val	Leu	Val	Arg	Trp	Leu	Gln	Gly	Ser	Gln	Glu	Leu	Pro	Arg	Glu	Lys
		165				170								175	
Tyr	Leu	Thr	Trp	Ala	Ser	Arg	Gln	Glu	Pro	Ser	Gln	Gly	Thr	Thr	Thr
	180					185						190			
Phe	Ala	Val	Thr	Ser	Ile	Leu	Arg	Val	Ala	Ala	Glu	Asp	Trp	Lys	Lys
	195					200						205			
Gly	Asp	Thr	Phe	Ser	Cys	Met	Val	Gly	His	Glu	Ala	Leu	Pro	Leu	Ala
	210				215					220					
Phe	Thr	Gln	Lys	Thr	Ile	Asp	Arg	Leu	Ala	Gly	Lys	Pro	Thr	His	Val
	225					230				235					240

Asn Val Ser Val Val Met Ala Glu Val Asp
245 250